

SEQUENCE LISTING

Applicant name : Japan Science And Technology Corporation  
Title of invention : Method for transforming plant, the resultant  
plant and gene thereof  
File reference : JA908155  
Application : International application filed on March 24, 1999  
Filing date : March 24, 1999  
Priority application : JP Patent application No. 10-96637  
Priority application filing date: March 24, 1998  
Number of SEQ ID Nos : 34

SEQ ID No.: 1  
Length : 2092  
Type : nucleic acid  
Strandness: double  
Topology : linear  
Molecular type: other nucleic acid  
synthetic DNA

Feature :  
Name/Key : modified base

SEQ :

GAATTCTCTA GACTCCACCA TGGTTAGAAC CAGAGTCCTT TTCTGCCTCT TCATCTCTTT 60

CTTCGCTACA GTCCAATCGA GCGCTACACT CATCTCCACT TCATGCATTT CTCAGGCTGC 120

ACTGTACCAG TTCGGATGCT CAAGCAAGTC AAAGTCTTGC TACTGCAAGA ACATCAATTG 180

GCTCGGAAGC GTCACTGCAT GCGCTTATGA GAACTCCAAA TCTAACAAGA CTCTGGACTC 240  
CGCTTTGATG AAACCTTGCCA GCCAATGCTC AAGTATCAAG GTTTACACAC TGGAGGACAT 300  
GAAGAACATC TACCTTAATG CAAGTAACTA CCTTCGCGCT CCTGAGAAAT CCGATAAGAA 360  
GACAGTTGTT TCACAACCGT TGATGGCAAA TGAGACGGCC TATCACTACT ACTATGAGGA 420  
AAACTATGGG ATCCACTTGA ATTTGATGCG ATCTCAATGG TGCGCATGGG GCCTCGTCTT 480  
CTTCTGGGTC GCAGTCCTTA CCGCCGCAAC TATCTTGAAC ATTCTCAAAC GCGTATTCGG 540  
CAAGAACATT ATGGCAAATT CTGTAAAGAA GTCTCTTATC TACCCAAGCG TTTACAAAGA 600  
CTACAACGAG AGAACTTTCT ATCTTTGGAA ACGTTTGCCA TTCAACTTTA CAACTCGAGG 660  
CAAAGGACTC GTAGTTCTTA TCTTTGTCAT TCTGACTATT CTCTCACTCT CTTTCGGACA 720  
TAACATCAAG TTGCCACATC CTTACGATAG ACCTAGATGG AGAAGATCAA TGGCATTTCGT 780  
CTCAGCCCGT GCTGACTTGA TGGCAATCGC TCTTTTCCCC GTGGTGTACC TTTTCGGTAT 840  
CCGGAACAAC CCCTTCATCC CAATCACCGG ATTGAGCTTT AGTACTTTCA ACTTTTACCA 900  
CAAATGGTCA GCATACGTCT GCTTCATGTT AGCCGTCGTC CATTCAATCG TTATGACCGC 960  
TTCAGGAGTT AAACGAGGAG TATTCCAGTC TCTTGTAAGG AAATTCTACT TCAGATGGGG 1020  
AATAGTAGCC ACAATTCTTA TGTCCATCAT CATTTTCCAG TCCGAGAAGG TCTTCAGGAA 1080

CCGAGGTTAT GAAATCTTCT TACTTATTCA CAAAGCCATG AACATCATGT TTATCATAGC 1140  
 TATGTATTAC CATTGCCACA CACTAGGATG GATGGGCTGG ATCTGGTCCA TGGCTGGCAT 1200  
 CCTCTGCTTC GACAGGTTCT GCCGAATTGT ACGTATCATC ATGAACGGAG GTCTTAAGAC 1260  
 CGCCACTTTG TCGACCACAG ATGATTCTAA CGTTATCAAG ATCTCTGTCA AGAAGCCTAA 1320  
 GTTCTTCAAG TATCAAGTGG GAGCATTGTC CTATATGTAC TTTCTTTCAC CAAAATCAGC 1380  
 CTGGTTCTAC AGTTTTCAAT CTCATCCCTT CACAGTCCTA TCAGAAAGGC ACAGAGATCC 1440  
 TAACAACCCA GATCAACTAA CTATGTACGT CAAAGCTAAC AAGGGCATTG CGAGAGTACT 1500  
 TCTTAGCAAA GTTCTAAGCG CTCCAAACCA TACCGTTGAT TGCAAGATTT TCTTAGAGGG 1560  
 ACCATATGGC GTAAGTGTCC CTCACATTGC CAAACTTAAG AGAAATCTAG TAGGAGTAGC 1620  
 TGCGGGCCTC GGCCTGGCAG CCATCTACCC CCATTTTCGTA GAATGCCTTA GATTGCCTAG 1680  
 CACTGATCAA CTGCAGCACA AGTTCTACTG GATCGTCAAC GACCTTAGTC ACCTTAAGTG 1740  
 GTTCGAAAAC GAGCTACAAT GGCTTAAGGA GAAATCTTGT GAAGTCTCTG TCATCTACAC 1800  
 TGGGTCATCA GTGGAGGATA CAAACTCAGA TGAGTCCACT AAGGGTTTCG ATGACAAGGA 1860  
 AGAATCTGAA ATCACCGTAG AATGCCTTAA CAAGAGGCCA GACCTCAAAG AGCTAGTGAG 1920  
 ATCAGAGATC AAATTGTCAG AACTCGAGAA CAACAACATC ACTTTCTACT CATGCGGACC 1980

AGCGACTTTC AATGACGACT TTAGGAATGC AGTTGTACAA GGTATCGATT CTAGTCTGAA 2040

GATAGATGTC GAACTAGAGG AGGAGAGTTT TACTTGGTAA GAGCTCAAGC TT 2092

SEQ ID No.: 2

Length : 687

Type : amino acids

Topology : linear

Molecular type: protein

Original Source

Organism : yeast

SEQ :

Met Val Arg Thr Arg Val Leu Phe Cys Leu Phe Ile Ser Phe Phe	15
Ala Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr Ser Cys Ile	30
Ser Gln Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys Ser Lys	45
Ser Cys Tyr Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr Ala	60
Cys Ala Tyr Glu Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala	75
Leu Met Lys Leu Ala Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr	90
Leu Glu Asp Met Lys Asn Ile Tyr Leu Asn Ala Ser Asn Tyr Leu	105

Arg Ala Pro Glu Lys Ser Asp Lys Lys Thr Val Val Ser Gln Pro	120
Leu Met Ala Asn Glu Thr Ala Tyr His Tyr Tyr Tyr Glu Glu Asn	135
Tyr Gly Ile His Leu Asn Leu Met Arg Ser Gln Trp Cys Ala Trp	150
Gly Leu Val Phe Phe Trp Val Ala Val Leu Thr Ala Ala Thr Ile	165
Leu Asn Ile Leu Lys Arg Val Phe Gly Lys Asn Ile Met Ala Asn	180
Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr Lys Asp Tyr	195
Asn Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe Asn Phe	210
Thr Thr Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile Leu	225
Thr Ile Leu Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His	240
Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met Ala Phe Val Ser	255
Arg Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro Val Val Tyr	270
Leu Phe Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr Gly Leu	285
Ser Phe Ser Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr Val	300
Cys Phe Met Leu Ala Val Val His Ser Ile Val Met Thr Ala Ser	315
Gly Val Lys Arg Gly Val Phe Gln Ser Leu Val Arg Lys Phe Tyr	330

Phe Arg Trp Gly Ile Val Ala Thr Ile Leu Met Ser Ile Ile Ile	345
Phe Gln Ser Glu Lys Val Phe Arg Asn Arg Gly Tyr Glu Ile Phe	360
Leu Leu Ile His Lys Ala Met Asn Ile Met Phe Ile Ile Ala Met	375
Tyr Tyr His Cys His Thr Leu Gly Trp Met Gly Trp Ile Trp Ser	390
Met Ala Gly Ile Leu Cys Phe Asp Arg Phe Cys Arg Ile Val Arg	405
Ile Ile Met Asn Gly Gly Leu Lys Thr Ala Thr Leu Ser Thr Thr	420
Asp Asp Ser Asn Val Ile Lys Ile Ser Val Lys Lys Pro Lys Phe	435
Phe Lys Tyr Gln Val Gly Ala Phe Ala Tyr Met Tyr Phe Leu Ser	450
Pro Lys Ser Ala Trp Phe Tyr Ser Phe Gln Ser His Pro Phe Thr	465
Val Leu Ser Glu Arg His Arg Asp Pro Asn Asn Pro Asp Gln Leu	480
Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr Arg Val Leu Leu	495
Ser Lys Val Leu Ser Ala Pro Asn His Thr Val Asp Cys Lys Ile	510
Phe Leu Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile Ala Lys	525
Leu Lys Arg Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val Ala	540
Ala Ile Tyr Pro His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr	555

Asp Gln Leu Gln His Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser	570
His Leu Lys Trp Phe Glu Asn Glu Leu Gln Trp Leu Lys Glu Lys	585
Ser Cys Glu Val Ser Val Ile Tyr Thr Gly Ser Ser Val Glu Asp	600
Thr Asn Ser Asp Glu Ser Thr Lys Gly Phe Asp Asp Lys Glu Glu	615
Ser Glu Ile Thr Val Glu Cys Leu Asn Lys Arg Pro Asp Leu Lys	630
Glu Leu Val Arg Ser Glu Ile Lys Leu Ser Glu Leu Glu Asn Asn	645
Asn Ile Thr Phe Tyr Ser Cys Gly Pro Ala Thr Phe Asn Asp Asp	660
Phe Arg Asn Ala Val Val Gln Gly Ile Asp Ser Ser Leu Lys Ile	675
Asp Val Glu Leu Glu Glu Glu Ser Phe Thr Trp ***	687

SEQ ID No.: 3

Length : 17

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

002260 092200

**U-P-O-E-A**

8 / 25



SEQ :

GAATTCTCTA GACTCCACCA TGGTTAGAAC CAGAGTCCTT TTCTGCCTCT TCATCTCTTT 60

SEQ ID No. : 6

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid

synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

GTCCAATCGA GCGCTACACT CATCTCCACT TCATGCATTT CTCAGGCTGC ACTGTACCAG 60

SEQ ID No.: 7

Length : 83

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid

synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

CAAGCAAGTC AAAGTCTTGC TACTGCAAGA ACATCAATTG GCTCGGAAGC GTCAGTGCAT 60

GCGCTTATGA GAACTCCAAA TCT 83

SEQ ID No.: 8

Length : 83

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid

synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

TCCAGTGTGT AAACCTTGAT ACTTGAGCAT TGGCTGGCAA GTTTCATCAA AGCGGAGTCC 60

AGAGTCTTGT TAGATTGGA GTT 83

SEQ ID No.: 9

Length : 83

Type : nucleic acid  
Strandness: single  
Topology : linear  
Molecular type: other nucleic acid  
synthetic DNA

Feature :  
Name/Key : primer bind

SEQ :

TGTCTTCTTA TCGGATTTCT CAGGAGCGCG AAGGTAGTTA CTTGCATTAA GGTAGATGTT 60

CTTCATGTCC TCCAGTGTGT AAA 83

SEQ ID No.: 10  
Length : 83  
Type : nucleic acid  
Strandness: single  
Topology : linear  
Molecular type: other nucleic acid  
synthetic DNA

Feature :  
Name/Key : primer bind

SEQ :

GGATCCCATTA GTTTTCCTCA TAGTAGTAGT GATAGGCCGT CTCATTTGCC ATCAACGGTT 60

GTGAAACAAC TGTCTTCTTA TCG 83

00000000000000000000000000000000

[illegible][illegible]

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000000000000000

[illegible]

00000000000000000000000000000000

00000000000000000000000000000000

[illegible]

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000000000000000

[illegible][illegible][illegible]

00000000000000000000

[illegible][illegible][illegible]

**00000000**

00000000000000000000





SEQ :

TAAAGTTGAA TGGCAAACGT 80

Name/Key : primer bind

**SEQ :**

CCGAAAGAGA GTGAGAGAAT 80

Type : nucleic acid

[illegible]

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

TCCGGATACC GAAAAGGTAC ACCACGGGGA AAAGAGCGAT TGCCATCAAG TCAGCACGGC 60

GTGAGACGAA TGCCATTGAT 80

SEQ ID No.: 17

Length : 83

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

TCCGGAACAA CCCCTTCATC CCAATCACCG GATTGAGCTT TAGTACTTTC AACTTTTACC 60

ACAAATGGTC AGCATACGTC TGC 83

**090762-00**

[illegible][illegible]

00000000000000000000000000000000

[illegible][illegible]

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000

[illegible]

00000000000000000000000000000000

00000000000000000000

00000000000000000000

00000000000000000000000000000000

[illegible][illegible]

00000000000000000000000000000000

[illegible]

00000000000000000000

[illegible]



TATTCCAGTC TCTTGTAAGG AAATTCTACT TCAGATGGGG AATAGTAGCC ACAATTCTTA 60

TGTCCATCAT CATTTTCCAG TCC 83

SEQ ID No.: 20

Length : 83

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid

synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

ATAAACATGA TGTTTCATGGC TTTGTGAATA AGTAAGAAGA TTCATAACC TCGGTTCTG 60

AAGACCTTCT CGGACTGGAA AAT 83

SEQ ID No.: 21

Length : 83

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid

synthetic DNA

Feature :



**SECRET**

CATAGCTATG ATAAACATGA TGT 83

Length : 83

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

CTGTCGAAGC AGAGGATGCC AGC 83

Length : 82

Strandness: single

**SECRET**

**SECRET**

**SECRET**

**SECRET**

**SECRET**

**SECRET**

**SECRET**

**SECRET**

**SECRET**

**SECRET**

**SECRET**

[illegible]

**SECRET**

**SECRET**

**SECRET**

**SECRET**



SEQ ID No.: 27

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

GGCCCGCAGC TACTCCTACT AGATTTCTCT TAAGTTTGGC AATGTGAGGG ACAGTTACGC 60

CATATGGTCC CTCTAAGAAA AT 82

SEQ ID No. : 28

Length : 82

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :

Name/Key : primer bind

[illegible]

# THE UNIVERSITY OF CHICAGO

CACGCCGAGG CCCGCAGCTA CT 82

Length : 77

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :

Name/Key : primer bind

SEQ :

GAGCTACAAT GGCTTAA 77

SEQ ID No. : 30

Length : 77

Type : nucleic acid

Strandness: single

Topology : linear

1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2

Name/Key : primer bind

ACAATGGCTT AAGGAGAAAT CTTGTGAAGT CTCTGTCATC TACACTGGGT CATCAGTGGA 60

GGATACAAAC TCAGATG 77

Length : 77

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :

Name/Key : primer bind

CAAAC TCAGA TGAGT CCACT AAGGG TTTCG ATGAC AAGGA AGAAT CTGAA ATCAC CGTAG 60

AATGCCTTAA CAAGAGG 77

SEQ ID No.: 32

Length : 77

Type : nucleic acid  
Strandness: single  
Topology : linear  
Molecular type: other nucleic acid  
synthetic DNA

Feature :  
Name/Key : primer bind

SEQ :

GTGATGTTGT TGTTCTCGAG TTCTGACAAT TTGATCTCTG ATCTCACTAG CTCTTTGAGG 60

TCTGGCCTCT TGTTAAG 77

SEQ ID No.: 33

Length : 77

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid  
synthetic DNA

Feature :  
Name/Key : primer bind

SEQ :

CGATACCTTG TACAACTGCA TTCCTAAAGT CGTCATTGAA AGTCGCTGGT CCGCATGAGT 60

AGAAAGTGAT GTTGTTG 77



SEQ ID No.: 34

Length : 77

Type : nucleic acid

Strandness: single

Topology : linear

Molecular type: other nucleic acid

synthetic DNA

Feature :

Name/Key: primer bind

SEQ :

AAGCTTGAGC TCTTACCAAG TAAAACTCTC CTCCTCTAGT TCGACATCTA TCTTCAGACT 60

AGAATCGATA CCTTGTA 77

00046025.092200